Amendments to the Specification:

Please replace the Title with the following amended Title:

Method, System, and Computer Software for Providing Information Related to Probe Sets Via a Genomic Web Portal

Please replace paragraph 0051 with the following amended paragraph:

Conventional Techniques for Obtaining Genomic Data: A number of conventional approaches for obtaining genomic data over the Internet are available, some of which are described in the book edited by Ouelette and Bzevanis, incorporated by reference above. Figure 3 is a functional block diagram representing one simplified example. As shown in Figure 3, user 101 may consult any of a number of public or other sources to obtain accession numbers 224'. As represented by manual operation 312, user 101 initiates request 312 by accessing through any web browser the Internet web site of the National Center for Biotechnology Information (NCBI) of the National Library of Medicine and the National Institutes of Health (as of January 2001, accessible at the Internet URL http://www.ncbi.nlm.nih.gov/). In particular, user 101 may access the Entrez search and retrieval system that provides information from various databases at NCBI . These databases provide information regarding nucleotide sequences, protein sequences, macromolecular structures, whole genomes, and publication data related thereto. It is illustratively assumed that user 101 accesses in this manner NCBI Entrez nucleotide database 314 and receives information including gene or EST sequences 316.

Particularly if accession numbers 224' represents a large number (e.g., one hundred) of

EST's or genes of interest, as may easily be the case following analysis of probe array

experiments, the tasks thus far described may take significant time, perhaps hours.

Please replace paragraph 0052 with the following amended paragraph:

User 101 typically copies sequence information from sequences 316 and pastes this

information into an HTML document accessible through NCBI's BLAST web pages 324

(as of April 2002, accessible at http://www.ncbi.nlm.nih.gov/BLAST/). This operation,

which also may be time consuming and tedious if many sequences are involved, is

represented by user-initiated batch BLAST request 322 of Figure 3. BLAST is an

acronym for Basic Local Alignment Search Tool, and, as is well known in the art,

consists of similarity search programs that interrogate sequence databases for both

protein and DNA using heuristic algorithms to seek local alignments. For example, user

101 may conduct a BLAST search using the "blastn" nucleotide sequence database.

Results of this batch BLAST search, represented by similar nucleotide and/or protein

sequence data 326, on occasion may not be available to user 101 for many minutes or

even hours. User 101 may then initiate comparisons and evaluations 332, which may be

conducted manually or using various software tools. User 101 may subsequently issue

report 334 interpreting the findings of the searches and positing strategies and

requirements for follow-on experiments.